Package 'geuvStore2'

October 17, 2019

Title demonstrate storage discipline for eQTL enumerations, revised

Version 1.14.0

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Description demonstrate storage discipline for eQTL enumerations and analyses based on a selection of GEUVADIS results

Suggests Homo.sapiens, knitr (>= 1.7), rmarkdown

Imports methods, gQTLBase

Depends BatchJobs, GenomicRanges

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LazyLoad yes

biocViews ExperimentData, SequencingData, MicroarrayData

VignetteBuilder knitr

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R topics documented:

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geuvStore2-package *demonstrate storage discipline for eQTL enumerations, revised*

Description

demonstrate storage discipline for eQTL enumerations and analyses based on a selection of GEU-VADIS results

Details

The DESCRIPTION file: This package was not yet installed at build time.

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This package illustrates an approach to managing large numbers of tests, in this case, eQTL association statistics and annotation. The idea is that the report is broken into small chunks, indexed by feature names and ranges, and can be filtered using parallel computing if desired.

The `makeGeuvStore2` function constructs the basic object for working with a subset of tests related to the GEUVADIS study [PMID 24037378].

Author(s)

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Examples

```
mm = makeGeuvStore2()
mm
data(geuvStore2Desc)
geuvStore2Desc # describes distributed computing resources used
```

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gv2pm *components for constructing the distributed store for the subset of eQTL association statistics based on GEUVADIS*

Description

gv2pm and gv2rm are used to index distributed GRanges objects; geuvStore2Desc is a serialized description of store contents. kpp is the vector of gene identifiers retained in this subset (about 5

Usage

```
data("gv2pm")
```

Format

A data frame with 920 observations on the following 2 variables.

probeid a character vector

jobnum a numeric vector

Examples

```
data(gv2rm)
gv2rm
```

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